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Evaluation of centrally tested swine with an animal model

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TABLE OF CONTENTS

LIST OF TABLES

INTRODUCTION

> With the idea that the genes of an individual are random ones of a population of genes with independence between loci, and the idea the environmental effects can be regarded as realizations of independent Gaussian random variables, we see that we have reduced the whole (genetic) theory to what we in statistics call mixed linear model theory. The outcome is that what is called the theory of animal breeding is reduced to theory of a mixed linear model with fixed effects and independent Gaussian random effects. (Kempthorne, 1988)

Mixed model theory has only recently been proposed for swine breeding data analysis (Carlson, 1980; Willham, 1982; Mabry and Benyshek, 1984; Wood, 1986). Since few on-farm performance records exist, central swine test station records of performance are available as a source of across farm comparisons. Researchers are using this data source to provide genetic evaluations to swine industry associations (Hudson and Kennedy, 1985a; Goodwin, 1988; Miller, 1988). Because of limited testing space some selection of pigs entered in the test stations must occur. The intensity and method of this selection is unknown. Mixed model methods under a selection model require exacting assumptions to be fulfilled if their solutions are to be best linear unbiased predictors of genetic merit (BLUP).

This thesis will characterize the structure of Minnesota swine central test station data and determine the feasibility of applying mixed model analysis for prediction of breeding values and estimation of genetic trend.

LITERATURE REVIEW

Mixed Model

Methods

Selection index methods (Hazel, 1943) have been the main tool used by animal breeders to incorporate relative information and/or multiple trait information in genetic evaluations (Weber, 1987). Carlson (1980) demonstrated mixed model methods were superior to selection indices and phenotypic records in evaluating swine central test data. Kiele et al. (1988) determined mixed model methods were superior to selection indices when evaluating swine field data.

Henderson (1963) proposed the use of mixed linear models to evaluate genetic merit. The equations he proposed considered environmental effects of herd-year-season to be fixed and the breeding values of the animals to be multivariately normally distributed random effects. The mixed model equations are of the general form:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

y = records of performance of an animal,

X = known incidence matrix relating records to unknown fixed effects in model,

b = vector of unknown fixed effect solutions,

Z = known incidence matrix relating animals to records,

u = vector of random effect solutions, usually breeding values or transmitting abilities,

e = vector of random residual effects.

Henderson (1973) explained the difference between best linear predictors (selection index) and best linear unbiased predictors (BLUP). The methods differ in the information which must be assumed known and in the properties of solutions. Fixed effects are assumed known without error in application of a selection index. This is rarely the true situation and gives biased predictors of genetic merit if a

selection index is used in the unknown situation. The advantage of BLUP over selection index is that fixed effects are estimated simultaneously with prediction of random effects. Fixed effect solutions are the best linear unbiased estimator (BLUE) of some estimable function of the fixed effects and predictors of random effects are best linear unbiased predictors (BLUP) of random effects in the model. Genetic and environmental variances and covariances must be assumed known and constant for selection index and BLUP. These variances and covariances must be known for an unrelated, unselected base population in linkage equilibrium from which the evaluated animals are derived. The mean breeding value of the base population must be zero.

Henderson's (1976a) discovery of a simple method to calculate the inverse of the additive genetic relationship matrix ($\mathbf{A}^{-1}$) allowed the inclusion of genetic relationships among animals in the mixed model equations. Inclusion of $\mathbf{A}^{-1}$ reduces prediction error variances and improves accuracy of evaluations (Henderson, 1975b).

Henderson (1974) described the flexibility of the mixed model approach for breeding value estimation. Many models may be possible with the choice depending on computational ease. Two models that generate the same first and second moments of the data are equivalent. He described the following features of the mixed model method:

1) evaluations are unbiased, i.e. the predictor and predictand have the same expected value;
2) evaluations have minimum variance of prediction errors;
3) the method is easy to learn for those familiar with least squares;
4) it is easy to modify if conditions change;
5) its properties are clearly defined;
6) it takes advantage of modern statistical computing techniques for linear models;

7) it yields variances of prediction errors;
8) it sometimes eliminates bias due to selection and culling and provides a mechanism for checking such bias.

Henderson (1974, 1985) summarizes with the following general advice for use of mixed models for genetic evaluations:

1) account for major sources of variance and bias with the simplest model possible;
2) if possible, write a model with mutually uncorrelated sets of variables;
3) be careful to check the rank of coefficient matrix;
4) consider use of iterative solution since diagonal elements of the coefficient matrix tend to be larger than off-diagonal elements in mixed model equations.

Henderson (1976b) proposed multiple trait models using additive genetic relationship matrices. Multiple traits may be separate traits or the same trait measured at different times such as first and second lactations of dairy cows.

Quaas and Pollak (1980) extended the concept of equivalent models to derive a reduced animal model (RAM) equivalent to a full animal model. Their motivation was to reduce the number of equations to be solved for a fixed number of animals. RAM models consist of a genotypic model for parents and a gametic model for progeny. RAM is equivalent to absorbing progeny records into their parent's records. This approach has been very successful in reducing the number of equations to be solved, especially in species that have more than one offspring per parity (Blair and Pollak, 1984b).

Schaeffer and Kennedy (1986) described an indirect method of solving mixed model equations. This indirect method does not require construction of the mixed model equations but instead makes use of successive adjustments to model effect means. The indirect method reduces computational costs and time when compared to absorbed models or RAM. Misztal and Gianola (1987) present the indirect approach in terms of successive

averaging with both Gauss-Seidel and Jacobi iteration. The indirect approach is also called iterating on data. Prediction error variances and accuracies for indirect approach solutions must be approximated as with other iterative solutions.

Genetic groups

Genetic groups are included in mixed models to account for different genetic subpopulations. The total genetic merit of an animal is a function of its genetic group and its deviation from that group (Henderson, 1959).

Bichard et al. (1973) discussed the selection errors possible when parents of animals to be selected belong to different genetic subpopulations. They derived methods of selection to allow for genetic group effects under some conditions.

Pollak and Quaas (1983) defined group effects as functions of genetic selection differentials, the function depending upon how $\mathbf{A}^{-1}$ is computed. The genetic selection differential was defined as the mean breeding value of the selected individuals minus the mean breeding value of the subpopulation from which they were selected. This definition is straightforward only in populations with discrete generations. Genetic groups are the accumulated genetic selection differentials. As $\mathbf{A}^{-1}$ becomes more complete, as in using an animal model instead of a sire model, the need for groups is reduced. The animal model adjusts each animal's breeding value for the genetic merit of its relatives. Theoretically, if all animals from the base population to current population are included in $\mathbf{A}^{-1}$ no genetic grouping is needed. The simulation results in this paper supported this hypothesis. Bichard et al. (1973) suggested not treating animals as members of genetic groups but to adjust each animal for the

accumulated selection differential of its own particular ancestors.

Famula (1985) demonstrated the equivalence between mixed models including groups and restricted BLUP models. He suggested regarding genetic groups as random effects since they are accumulated selection differentials which are functions of random genetic effects. Groups account for selection by "breaking" the correlation between the predictor of genetic merit ($\hat{\mathbf{u}}$) and the effects of selection as reflected in the selection differentials. Genetic groups are a means of correcting genetic merit predictors so that the selection criterion is not correlated with changes in genetic means imposed by selection.

A further extension of the grouping strategy is to assign any unidentified parent to a genetic group based upon some characteristic of its progeny. This strategy creates "phantom groups" for unidentified parents. There may be separate groups for sires and dams if the data indicate them appropriate. All unidentified parents are considered to come from the original base population if genetic groups are not included in the mixed model. This is incorrect if unidentified parents come from different generations and there is genetic trend in the population. The use of $\mathbf{A}^{-1}$ and phantom groups should account for most changes due to selection (Robinson, 1986; Westell et al., 1988; Quaas, 1988). Phantom groups are composed of unidentified ancestors that have geen grouped by some characteristic of their descendants.

There are no general rules for definitions of groups for models. Quaas and Pollak (1987) suggest animal's date of birth, its progeny's date of birth, and sex of animal as possible grouping strategies. They also caution against having too many genetic groups in a model since confounding with other fixed effects may result.

Selection models

An additive genetic mixed model assumes that the random part of an animal's record is the sum of a random breeding value and a random environmental deviation. Furthermore, these two random variables are assumed uncorrelated. The records used in an evaluation are assumed to be a random sample of a larger population.

Culling of animals based on initial performance creates a biased evaluation when the animals' later records are the basis of evaluation. Henderson et al. (1959) derived mixed model estimators of genetic merit for evaluating first and second lactations of dairy cows sequentially culled on first lactation records. This method is unbiased if repeatability is known.

Henderson (1965) realized that animal breeding data, particularly industry data, were likely to reflect selection on genetic merit. He derived the **L** matrix of selection, which requires knowledge of the form of the selection used. This **L** matrix consists of orthogonal contrasts which describe the selection process. Henderson (1975a) expanded on the **L** matrix concept as it applied to selection on the data ($\mathbf{y}$), predictors of genetic merit ($\hat{\mathbf{u}}$), and environmental deviations ($\hat{\mathbf{e}}$). He proposed deriving unbiased predictors from a model conditional on selection of certain linear functions of random variables jointly distributed with the random variables of the usual mixed model.

Henderson (1985) listed these requirements of the selected data to produce BLUP:

1) the random variables have a multivariate normal distribution;
2) genetic and environmental variances and covariances are known to proportionality;
3) selection decisions were based on linear translation invariant functions of the data;

4) the data used in selection decisions are available and are included in the mixed model equations.

Henderson (1980) described the conditions for $\mathbf{L'X=0}$ to satisfy requirement 3. If selection decisions are made within fixed effects, year-season for example, then $\mathbf{L'X=0}$. If breeders select on linear functions of the data ($\mathbf{y}$) that have been adjusted for fixed effects ($\hat{\mathbf{b}}$) using estimators that are unbiased in the no selection model then $\mathbf{L'X=0}$ and BLUP will result from mixed models. This allows the use of selection models when selection decisions are based upon reported breeding values if the data the breeding values are predicted from are included in the selection model. Gianola et al. (1988) found that stabilizing selection did not bias BLUP evaluations.

Goffinet (1983) discussed sequential selection with two traits where selection was done upon the genetic merit of the first trait and genetic merit predictors are desired for the second trait. A multitrait model was used to predict genetic merit. If all information related to the two sets of records is used and knowledge of the exact selection method used for the first trait is available, BLUP of the second trait remains unbiased. The first trait selection must be made according to an invariant criterion with respect to fixed effects.

Pollak and Quaas (1981) simulated beef cattle weaning and yearling weight records to compare the results of mixed model evaluations of yearling weight data with and without selection on weaning weight. Their evaluations based on selected records were consistently biased for parents and progeny. Poor animals were overevaluated and superior animals were underevaluated. The bias was largest in the extremes of performance. When records of the weaning weight selection were included in a multiple trait model, the yearling weight evaluations were unbiased. Pollak et al. (1984) verified the selection bias caused by ignoring selected records by applying

a multiple trait model to weaning weight and postweaning gain in beef cattle. Use of the multiple trait model produced unbiased evaluations for postweaning gain. When a sire's progeny were culled based on poor weaning weight the sire was overevaluated for postweaning gain in a single trait model.

When selection is known to have occurred and genetic relationships do not extend to the unselected base population Henderson (1985) suggested the use of an altered genetic relationship matrix to produce BLUP. This altered matrix would consider the first known animals as fixed, using the identity matrix as the relationship matrix for these base animals. The resulting equations do not allow use of the simple $\mathbf{A}^{-1}$ calculation method and are computationally difficult. It is also not clear what is being predicted under some models. Henderson (1988) developed a simpler method to find the altered $\mathbf{A}^{-1}$ based upon his simple method of calculating $\mathbf{A}^{-1}$.

Estimation of genetic trend

Henderson (1973) recommended mixed model methods for the estimation of genetic and environmental performance trends as well as breeding value estimation. The following conditions must hold:

1) multivariate normal distribution of random genetic effects;
2) additive genetic model;
3) inverse of the additive genetic relationship matrix includes all base population animals and all descendants of the base population animals;
4) selection is by translation invariant linear function and all records used in making the selection decisions are included in the equations;
5) additive genetic and environmental variances and covariances are known and constant.

Implicit in these conditions is the use of Bulmer's (1971) additive genetic infinitesimal loci model. Only with this model do conditions 1 and 5 hold. The infinitesimal model assumes no epistasis, linkage equilibrium in the base population, independently distributed environmental deviations, and an infinitely large number of loci controlling the trait of interest. For a fixed amount of heritable variation the intensity of selection at each locus is proportional to the number of loci. As the number of loci approaches infinity selection no longer changes allele frequencies.

Changes in genetic variance are due to changes in allele frequencies and linkage disequilibrium (Lush, 1945). Additive genetic value of a genotype is a statistical abstraction, not biological fact. It is a property of the genotype, which is constant, and the population, which changes with selection (Kempthorne, 1960). Selection that leads to allele frequency changes produces additive genetic variances which are very difficult to assess. The correct additive genetic variance and heritability for a population continually under selection would tend to be one generation different than the population you wish to evaluate (Robertson, 1977). Invoking the infinitesimal model reduces any changes in additive genetic variance to changes in linkage disequilibrium.

Linkage disequilibrium exists when the genotype frequencies at two or more loci considered jointly are not what would be expected from allele frequencies. These loci have a covariance which may be negative or positive (Falconer, 1981). Thomson (1977) defined linkage disequilibrium as the nonrandom association of alleles at two or more loci. The coefficient of disequilibrium is the difference between the frequency of a gametic type and the product of the frequencies of the alleles in the gamete.

Thomson (1977) listed five causes of linkage disequilibrium:

1) stabilizing, directional, or disruptive selection;
2) migration and admixture of genetically different populations;
3) genetic drift;
4) inbreeding;
5) selection operating on a closely linked locus.

Directional selection, as in animal breeding, always produces negative linkage disequilibrium which reduces additive genetic variance (Hill and Robertson, 1966). Recombination of genomes breaks up some disequilibrium each generation so that after two or three generations of selection the additive genetic variance stabilizes if intensity of selection remains constant. The decrease in additive genetic variance due to linkage disequilibrium reduces h^2 below the value of the base population in linkage equilibrium and so reduces response to selection (Bulmer, 1971). Fimland (1979) states that genetic parameters based on the stabilized selected populations are the parameters of choice for predicting genetic merit. He did not propose these parameters for mixed models.

Cockerham (1956) proved that if position effects are absent the covariances between parent and offspring are unaffected by linkage. For example, with two loci the coupling and repulsion parents have identical genotypic values. The distribution and mean of their offspring as a group doesn't depend upon linkage. The average crossproduct between parent and offspring remains the same as if there were no linkage. Schnell (1963) confirmed that only parent-offspring covariances were unaffected. Collateral relatives and ancestors or descendants more than one generation removed from an animal have altered genetic covariances due to linkage disequilibrium. Bulmer (1976) found the joint distribution of a metric character in the presence of linkage is multivariate normal only for parent and progeny.

Henderson (1976a) used Cholesky decomposition (Jennings, 1977) to reduce the additive genetic relationship matrix (**A**) to the product of lower and upper triangular matrices (**LL'**). These triangular matrices **L** and **L'** are not the **L'** matrix of selection defined for selection models. Henderson further reduced **L** to the product of a lower triangular matrix **T** and a diagonal matrix **D**. **T** is equal to **L** except the diagonal elements of **T** are unity. **D** is a diagonal matrix consisting of the diagonal elements of **L**. Therefore **A** = **TDDT'**. Henderson's simple method of $\mathbf{A}^{-1}$ calculation ignores inbreeding effects upon **DD**. Quaas (1976) derived a simple method of $\mathbf{A}^{-1}$ calculation that accounts for inbreeding effects on the coefficients of **DD**. Thompson (1977) showed the triangular matrix **T** was the gene flow matrix from the base population. Kennedy and Sorensen (1988) defined **A** as the product of **TWT'** where **T** is the lower triangular gene flow matrix, **W** is a diagonal matrix of coefficients of Mendelian sampling variance equivalent to Henderson's **DD**, and **T'** is the upper triangular gene flow matrix. Breeding values (**u**) may be represented as **u** = **TW**, a linear function of breeding values from the base population and Mendelian sampling terms. Since **T** relates parents to progeny it is unaffected by linkage disequilibrium if both parents are known. The Mendelian sampling coefficients of **W** are unaffected by selection or linkage disequilibrium. This gives the result that the **A** matrix is unaffected by linkage disequilibrium if **A** is complete to the base population. If one or both of the parents are unknown the elements of **W** include contributions of variances of the unknown parents plus Mendelian sampling. These coefficients are unaffected by selection only if the unknown parents are unselected.

Changes in genetic variance among animals due to inbreeding can also be accounted for by the **A** matrix. The coefficients in **W** are $.25*(3-F_p)$ when one parent is known where F_p is the

inbreeding coefficient of the known parent and .5*(1-$\bar{F}$) if both parents are known where $\bar{F}$ is the mean inbreeding coefficient of the animal's parents. Changes in genetic variance due to genetic drift are similarly accounted for in **A** (Sorensen and Kennedy, 1983).

Blair and Pollak (1984a) use mixed model methods to estimate genetic trends in sheep with and without control populations. They concluded that for the mixed model approach to work without a control population 'fairly strong' genetic ties among years are required. No definition of 'fairly strong' was given.

Berger et al. (1987) partitioned genetic and environmental trends in Tribolium with a mixed model without the use of a control population. A complete $\mathbf{A}^{-1}$ was used and pedigrees were complete back to an unselected base population.

Heterogeneous variance

Mixed model analysis of animal breeding data assumes fixed effects have equal variances but may have different means. A positive relationship between mean and variance tends to spread the breeding values more in higher mean contemporary groups. Animals represented in these higher mean variance contemporary groups may be overevaluated while animals in lower mean-variance contemporary groups may be underevaluated (Vinson, 1987). If the mean and variance within contemporary group are related the estimated breeding value of an animal may be a function of group variance as well as genotype and so may be misranked. Transformation of records to reduce contemporary group mean-variance relationships may lead to more accurate evaluation of breeding values. Estimation of genetic and environmental variance components is recommended to determine the stability of heritability estimates (Boldman, 1989). Central test station data are generally poorly suited for variance component estimation due to possible selection

bias and small numbers of animals tested in each contemporary group.

Central Test Station Programs

Central test stations accept young pigs of known parentage from breeders and record performance for economically important traits to a weight endpoint, usually the current desired pork industry market hog weight. The first swine test stations were built in Denmark in 1907 for carcass evaluation. The central station concept of swine improvement was first adopted in the U.S.A. by Ohio producers in 1954 and Iowa producers in 1956 (Craft, 1960). The Minnesota station was built in 1958 (Christians, 1982).

The goals of central test station programs are to educate producers about performance testing methods, provide boars to commercial pork producers, and make genetic change in the swine population (Robison, 1982).

Central testing is appropriate if there are no carryover effects of pre-test environment on station performance, genotype by environment interactions between station performance and on-farm performance do not exist, test conditions are uniform for all pigs, and representative samples of pigs are tested (King, 1955).

The three programs that are used in swine central test stations are progeny test to select parents, sib test for the selection of full or half sibs of animals tested, and record of performance for selection of tested animals (King, 1955).

U.S. test stations are unusual in not imposing any form of required testing or breeding structure. The initial European programs were based on a clearly defined selection goal, required testing, and imposed breeding structure (Robison, 1982). Stations in the U.S. have open entry policies, requiring only known parentage and entry weight limits (Weber, 1987). Breeder selection of litters and pigs within litter to

enter test may create an unknown bias due to differences between breeders' ability to predict future performance of pigs (King, 1955). Smith (1960) recommended reserving station space exclusively for nucleus herds to maximize genetic progress in the swine population.

Swine breeders in the U.S. were initially supportive of central test stations because they felt test stations gave them uniform and accurate data for selection purposes. These breeders also discovered that superior performance by a small number of their boars' progeny at the test station allowed them to charge premium prices for their on-farm production (Boucher, 1962). More recently breeder interest in central testing has declined. It has become a relatively expensive program with poor organization and leadership leading to the perception of little relevant progress (Miller, 1983).

Genotype by Environment Interaction

> In the broad sense there are no independent genetic and environmental variations in animal performance. Any phenotypic expression of the genotype requires a relatively specific sequence of environments and any environmental influence is measurable only as it changes the expression of viable genotypes. (Dickerson, 1962)

Central test stations give tested animals a more specialized environment than breeders are able to give their larger groups of animals on the farm. The competitive environment of larger groups of animals per pen may promote more expression of different genotypes than the relatively isolated environment of the test station (Griffing, 1977). Lush (1945) stated that the breeder should keep his animals under the environment they and their descendants are intended to be used so desired genes may express their effects and be selected. Information about the relative magnitude of different sorts of genetic variance obtained from an experiment confined to one of many possible environments needs to be supplemented by some information

about the magnitude of bias from genotype by environment interaction variance (Comstock, 1960).

Falconer (1952) considered the same measurements taken in two different environments as two genetically correlated traits. Central testing programs assume a genetic correlation of one between test station performance and on-farm performance (Steane, 1981).

Bampton et al. (1977) found no genotype by environment interaction in British swine data. Sex of tested animal was confounded with environment and dams of equal merit were assumed in their study. They found that sires with progeny in both test stations and on-farm tests tended to have higher station scores indicating top sires at the station were more widely used in industry. Assumptions of random sampling of entries to the station and random mating to dams could not be verified.

Kuhlers et al. (1977b) found no rank changes among sires due to genotype by environment interaction for production and carcass traits in on-farm records.

Standal (1977) found differences in backfat depths between station and farm were due to measurement differences between ultrasonic and carcass methods. His results suggested genotype by environment interaction for weight gain.

Roberts and Curran (1981) found station mean performance to be superior to on-farm performance. They concluded the two programs were selecting similar, if not identical, aggregate genotypes.

Merks (1986) found no genotype by environment interactions between station and on-farm performance in Dutch Landrace and Yorkshires.

Herd of Origin Effects

If pre-test environment effects carry over to influence station performance the results will be biased (King, 1955).

Jonsson and King (1962) concluded pre-test environment was not a significant source of variation in British test station data. Cox and Smith (1968) found environmental herd effects in Iowa central test data and suggested they could be due to pre-test environment or selection of entries. Kennedy and Quinton (1987) found differences due to herd health influenced on-farm performance but not station performance for daily gain and backfat depth.

A maternal effect is a phenotypic value of a dam measurable only as a component part of her offspring's phenotypic value. If there is a negative correlation between direct and maternal effects selection on phenotype is difficult (Willham, 1972).

Kuhlers et al. (1977a) found no maternal or grandmaternal additive genetic effects on weight gain. Bereskin (1984) found no significant genetic correlation between sow productivity index and daily gain or backfat depth.

Skjervold and Standal (1964) compared on test performance of pigs weaned at five or eight weeks of age. Pigs weaned at eight weeks grew more rapidly to 20 kg body weight but pigs weaned at five weeks of age grew more rapidly on test. Webb and King (1979) compared performance of pigs weaned at three, five and eight weeks of age. Carcass traits were not influenced by weaning age. On test growth rates increased with increasing age at weaning. The authors concluded that biased evaluations may result if a wide range of weaning practices are used by breeders.

Standal (1973) found pigs from first female parity litters grew more slowly than pigs from later parity litters. Willeke and Richter (1979) found pigs from first female parity litters grew more slowly and were leaner than pigs from later parity litters. Pigs raised in litters of nine or more pigs grew more slowly than pigs raised in smaller litters.

Van der Steen (1982) standardized litter sizes at birth to six or twelve nursing pigs. He concluded gilts from large

litters grew more slowly and were leaner than gilts raised in small litters.

McKay and Garnett (1986) concluded that crossfostering of piglets from one litter to another will not seriously bias performance testing results because postnatal effects are minor relative to direct additive genetic effects for postweaning growth rate and probe backfat thickness.

Adjustment Factors

Swine carcass traits are generally adjusted to a constant body weight basis. Daily gain on test may be adjusted for initial weight and final weight. Cox (1963) found breed differences in adjustment factors for average backfat depth. Bruner and Swiger (1968) found significant sex and sex by breed interaction effects in Ohio swine test station data. They recommended using breed specific sex adjustments. Hetzer and Miller (1972) found breed differences between daily gain and backfat depth correlations. McKay and Garnett (1988) found interactions with breed, season, and sex for the regression of probed backfat depth on body weight. Goodwin et al. (1987) found breed, sex and initial weight effects on central test station performance but no breed by sex interactions. McKay and Rahnefeld (1986) recommended selecting pigs using adjustment factors for sex pooled across breeds rather than separate sex parameters even if genotype by sex interactions are found. Weber (1987) recommends uniform adjustment factors for all breeds and sexes.

Methods of Genetic Trend Estimation in Swine

The estimation of response to selection and genetic trend is necessary if choices among selection methods are to be made correctly. The estimation of trend or response in populations undergoing selection has been attempted by several methods.

Goodwin et al. (1960) planned a mating design for chickens that relied upon repeat matings across two year periods. This design accounted for parity effects of the dams.

Smith (1962) proposed evaluating swine test station data based on comparisons of sires having progeny in subsequent test periods. This method assumes no preselection of sires for progeny test, no differential matings following initial genetic evaluations, no age of sow or parity effects on progeny performance, use of the boars over relatively long periods of time, and correction of records for fixed effects influencing a trait. He cautioned that selection of sires and dams of tested animals on genetic merit would bias estimates of genetic change.

Cox and Smith (1968) measured genetic trend as twice the regression of progeny performance on age of dam within farrowing period. Parity of sow effects were confounded with trend estimates. This method was used in a designed experiment.

Standal (1979) measured genetic trend in Norwegian Landrace test station records. A control herd submitted pigs to the station along with the nucleus breeders. He used least squares within sire regressions to measure trend.

Mitchell et al. (1982) measured genetic trend in British test station records. Two control herds submitted pigs to the station along with the nucleus breeders. Genetic change was estimated as the linear regressions on time of the differences between control groups and their contemporary groups from nucleus breeders of the same breed.

Lundeheim and Eriksson (1984), Kennedy et al. (1986) and Blanchard (1986) applied mixed model methods to swine test station data to estimate genetic trends.

MATERIALS AND METHODS

Data Source

Records of 1944 purebred Hampshire barrows and gilts centrally tested in the Market Progeny Pen Program at the Minnesota Swine Evaluation Station, New Ulm, MN, during 1963-1980 were evaluated in this study. These animals represent 402 sires and 1187 dams. Four generation pedigrees were obtained from the Hampshire Swine Registry, Peoria, IL. Pedigree records were unavailable for pigs tested after 1980. Complete pedigrees were found for 1498 pigs, while an additional 388 pigs have one parent pedigree available. Identification number of unknown parents was coded to identify full and half sibs within an entry for breeding value estimation. Herd of origin was recorded for 1920 pigs. Seventy-five different herds entered pigs in the station. Twenty-one herds were represented by single entry pens. Animals were tested in fall or spring seasons each year. No changes have been made to the Minnesota central test station since its construction in 1958. Diets fed were constant throughout the 1963-1980 period. All breeds were tested each year-season but only Hampshire data is evaluated here.

Definition of Variables

Average daily gain (ADG) of a pig is the total weight gain on test divided by the total number of days on test reported in kg/day.

Average carcass backfat depth (ABF) of a pig is the mean of midline carcass backfat measurements at the first rib, last rib, and last lumbar reported in mm.

Longissimus muscle area (LMA) of a pig is measured between the tenth and eleventh ribs in square centimeters.

Carcass length (LENGTH) of a pig is measured from the anterior of the first rib to the anterior point of the aitchbone in cm.

Generation interval (GI) of a pig is the age of its parents when it is born in years (Falconer, 1981).

Herd of origin (HERD) is the breeder herd that enters the pig in the station.

Sex of the pig (SEX) is either barrow or gilt.

Year season of test (CG) is the year-season, fall or spring, a pig was evaluated. This is the fixed environmental effect included in the reduced animal models.

Records

Information included on each pig tested includes birth date, sex, sire registration number, dam registration number, CG, ADG, LMA, LENGTH, and ABF.

Three generation pedigree records of sires and dams obtained from the Hampshire Swine Registry included birth dates and the owners of the sires and dams.

HERD of the entries was determined from pedigree ownership records and cross checked with 1963-1981 issues of the American Hampshire Herdsman. Owner of the dams of a sire group was determined to be the herd of origin when a sire was owned by two or more breeders.

ABF, LMA, and LENGTH were adjusted with National Swine Improvement Federation procedures to a constant weight of 105 kg (Weber, 1987). Gilt records of ADG, ABF, LMA, and LENGTH were adjusted to a barrow equivalent for reduced animal model breeding value estimation (Goodwin et al., 1987). Adjustment factors are shown in the Appendix.

Minnesota Market Progeny Pen Program

A market pen entry consists of four pigs sired by the same boar, and having no more than two pigs from the same litter.

Two or more pigs must be barrows. The entries are selected by the breeder and delivered to the station before they are 70 days of age. At entry pigs must weigh 16 to 25 kg (35 to 55 lbs). Pigs are placed on test when the four pigs' mean weight is 27 kg (60 lbs). Entries are penned in 1.8 x 3.3 m (6 x 11 ft) solid concrete floor bedded pens. An 18% protein pelleted corn-soybean meal diet is fed ad libitum for 30 days. A 16% protein pelleted corn-soybean meal diet is fed ad libitum from day 31 of test until pigs are removed from test at a weight of 105 kg (230 lbs). The end point of the test changed from 91 kg to 100 kg to 105 kg during the years 1963-1980.

Average daily gain and feed efficiency performance were recorded at the station. Off-test pigs were delivered to Geo. A. Hormel Co., Austin, MN for carcass evaluation. In addition to ABF, LMA and LENGTH the carcass measurements of lean percentage, ham weight, muscle quality scores, and tenth rib off midline backfat were taken, however, none of these additional measurements were taken throughout the 1963-1980 period. Various indexes combining growth and carcass traits were used during the 1963-1980 period to rank sire progeny market pen entries. Results of the Market Progeny Pen Program were published in the Minnesota Pork News, Hormel Farmer, and purebred association publications (Christians, 1982).

Statistical Analysis

Statistical model 1 is:

$$y_{ijklm} = \mu + CG_i + S_j + (CG*S)_{ij} + SG_k + DG_l + (SG*DG)_{kl} + b(W_{ijklm} - \bar{W}) + e_{ijklm}$$

y_{ijklm}= record of the m^{th} animal in the i^{th} year-season of the j^{th} sex, with the ij^{th} year-season by sex interaction, from the k^{th} sire group, from the l^{th} dam group, with the kl^{th} sire group by dam group interaction and $ijklm^{th}$ off-test weight,

μ = population mean,

CG_i = fixed effect of the i^{th} year-season contemporary group,

S_j = fixed effect of the j^{th} sex,

$(CG*S)_{ij}$ = fixed year-season by sex interaction,

SG_k = fixed effect of the k^{th} sire entry group,

DG_l = fixed effect of the l^{th} dam entry group,

$(SG*DG)_{kl}$ = fixed sire entry group by dam entry group interaction,

b = regression coefficient of the $ijklm^{th}$ record on $ijklm^{th}$ off-test weight,

W_{ijklm} = off-test weight of the m^{th} animal,

e_{ijklm} = m^{th} random residual.

ADG, ABF, LMA and LENGTH were analyzed with this model. Analyses were performed using SAS procedure GLM (SAS Institute Inc., 1985a, 1985b).

Statistical Model 2 is:

$$Y_{ijklm} = \mu + CG_i + S_j + (CG*S)_{ij} + H_k + F_{kl} + b(I_{ijklm} - \bar{I}) + e_{ijklm}$$

where

Y_{ijklm} = record of the m^{th} animal in the i^{th} year-season of the j^{th} sex, with the ij^{th} year-season by sex interaction, from the k^{th} herd of origin, sired by the l^{th} sire within the k^{th} herd with the $ijklm^{th}$ mean parental generation interval,

μ = population mean,

CG_i = fixed effect of the i^{th} year-season group,

S_j = fixed effect of the j^{th} sex,

$(CG*S)_{ij}$ = fixed year-season by sex interaction,

H_k = fixed effect of the k^{th} herd of origin,

F_{kl} = fixed effect of the l^{th} sire in the k^{th} herd of origin,

b = regression coefficient of the m^{th} record on the mean parental generation interval,

I_{ijklm} = mean parental generation interval of the m^{th} pig,

e_{ijklm} = m^{th} random residual.

Traits analyzed with this model were ADG, ABF, LMA, and LENGTH. Analyses were performed using SAS procedure GLM (SAS Institute Inc., 1985a, 1985b).

Breeding Value Estimation

Breeding values for genetic trend estimation were derived from a RAM. The computer programs for these analyses were obtained from the Animal Breeding Statistical Library (Berger and Healey, 1986). The RAM used was:

$$\begin{bmatrix} \mathbf{y}_p \\ \mathbf{y}_n \end{bmatrix} = \begin{bmatrix} \mathbf{X}_p \\ \mathbf{X}_n \end{bmatrix} \mathbf{b} + \begin{bmatrix} \mathbf{Z}_p \\ \frac{1}{2}\mathbf{P}_n \end{bmatrix} \mathbf{u}_p + \begin{bmatrix} \mathbf{e}_p \\ \boldsymbol{\phi}_n + \mathbf{e}_n \end{bmatrix}$$

$$\text{Var} \begin{bmatrix} \mathbf{e}_p \\ \boldsymbol{\phi}_n + \mathbf{e}_n \end{bmatrix} = \begin{bmatrix} \mathbf{I} & \mathbf{0} \\ \mathbf{0} & (\sigma_a^2/\sigma_e^2)\mathbf{D}_n + \mathbf{I} \end{bmatrix} \sigma_e^2$$

$$\text{Var}(\mathbf{u}_p) = \mathbf{A}_{pp}\sigma_a^2$$

$\mathbf{y}_p$ = vector of records of parents,

$\mathbf{y}_n$ = vector of records of progeny,

$\mathbf{X}_p$ = known incidence matrix of parental fixed effects,

$\mathbf{X}_n$ = known incidence matrix of progeny fixed effects,

$\mathbf{b}$ = vector of solutions for fixed effects,

$\mathbf{Z}_p$ = known incidence matrix of parents,

$\mathbf{P}_n$ = known matrix relating progeny to parents,

$\mathbf{u}_p$ = unknown vector of breeding values of parents,

$\mathbf{e}_p$ = unknown vector of random residuals for parents,

$\mathbf{e}_n$ = unknown vector of random residuals for progeny,

$\boldsymbol{\phi}_n$ = Mendelian sampling deviation of progeny,

$\mathbf{A}_{pp}$ = additive genetic relationship matrix of ancestors,

$\mathbf{D}$ = diagonal matrix of Mendelian sampling coefficents,
σ_a^2 = additive genetic variance in base population,
σ_e^2 = error variance.

Predicted breeding values of nonparent animals were obtained by equations (5) and (6) in Berger and Healey (1986).

Heritability of .40 was used for ADG estimation and .50 for ABF, LMA, and LENGTH (Ollivier and Sellier, 1982).

The fixed effect in the RAM was the year-season of test (CG). Pen effects within CG were confounded with sire effects because progeny of a sire were tested in the same pen.

Three RAM models were used, identical but for the amount of pedigree information included. The $\mathbf{A}^{-1}$ was extended to include grandparents and great-grandparents. The three models are:

1) all known ancestors of tested animals;
2) grandparents of tested animals who are not parents of tested animals and parents of tested animals;
3) only parents of tested animals.

The pedigree information was incomplete for animals born after 1976. The unknown pedigree information led to confounding genetic groups with CG. Parents with unknown birth years were assumed to be one year older than their progeny.

Genetic groups were defined as sire birth year and dam birth year. Unsuccessful attempts were made to solve RAM including both sire and dam birth year groups, sire groups only, and sire groups incremented by 2 years only.

RESULTS AND DISCUSSION

Inbreeding of Tested Animals

Inbred animals may display poorer performance than noninbred contemporaries (Falconer, 1981). Use of a complete relationship matrix in mixed model evaluations correctly allocates additional genetic variance among all animals but does not adjust for changes in level of performance (Henderson, 1963).

A computer program obtained from the Animal Breeding Statistical Library was used to calculate inbreeding coefficients (Berger and Healey, 1987). The level of inbreeding among the 1944 tested animals is shown in Table 1. Inbreeding coefficients were grouped into 5 levels by .05 increments. The relationship matrix inverse algorithm used to build $\mathbf{A}^{-1}$ for RAM to predict breeding values accounted for changes in additive genetic variance caused by inbreeding. The low levels of inbreeding found did not indicate adjustment of performance records for inbreeding coefficient (Blanchard, 1986).

Table 1. Inbreeding of tested animals

Inbreeding coefficient	No. pigs
0	1772
0.00 - 0.05	133
0.05 - 0.10	27
0.10 - 0.15	3
0.15 - 0.20	4
0.20 - 0.25	5
	1944

Sampling of Parents of Tested Animals

Mixed model breeding value estimation procedures for central test data assume a random sampling of possible parents is represented by the data.

Table 2 displays the generation interval groups of the parents of 1498 tested pigs with both parents' age known. Parents whose generation interval is less than 1.3 years are assumed to be young sires and dams in their first season of production with possibly their own performance record but no progeny information. Parents with a generation interval of more then 1.3 years but less than 1.8 years may be assumed to have progeny information on their first group of progeny. Parents with a generation interval greater than 1.8 years may be assumed to have progeny information from two or more groups of progeny.

Table 2. Number of pigs by generation interval of their parents

Sire's	Dam's generation interval			
generation interval[a]	<1.3 yrs	1.3-1.8 yrs	>1.8 yrs	Total
<1.3 yrs	416	136	215	767
1.3 - 1.8 yrs	59	147	184	390
>1.8 yrs	22	43	276	341
Total	497	326	675	1498

[a]Generation interval is the age of the parent when its progeny was born in years.

Assortative mating by age is evident in Table 2. A chi-square analysis (Snedecor and Cochran, 1980) of the mating frequencies of parent age groups assuming random mating rejected the hypothesis of random mating between age groups of parents. The mating structure of age groups in Table 2 is expected, however, if breeding herd management practices and

the increased physical size of the boars and sows as they become older are considered. Smith (1963) found 80% of the sires and 67% of the dams of British test station entries were less than two years old when their tested progeny were born. Kennedy et al. (1986) reported Canadian Hampshire sire generation intervals averaged 1.9 years and dam generation intervals averaged 2.1 years. Fredeen (1984) estimated average generation intervals in Canadian breeds to be 2 years. Table 2 suggests the need for different genetic groups among the parents of tested animals if there is genetic trend in the population.

Table 3 describes the generation interval of the parent when they were first represented by test station progeny. Sires and dams were each divided into two groups. Group 1 included sires or dams that had progeny tested in their first parity as defined by GI less than 1.3 years. Group 2 included sires and dams that were first represented by tested progeny in their second or later parities, GI greater than 1.3 years.

Table 3. Generation interval group of parent when first progeny entered the station

	No. Sires	No. Dams
Group 1	239 (53)[a]	337 (30)
Group 2	112 (10)	504 (43)
Total	351 (63)	841 (73)

[a]Number of parents represented again by progeny in subsequent test seasons.

Records of 1391 tested animals for which both sire and dam ages were known were analyzed with statistical model 1. Only sires and dams born in 1962 or later were represented. All parents represented had an opportunity to have been

progeny tested in first and later parities. The analysis of variance of statistical model 1 is shown in Table 4. Effects of CG, sex, and regression on off-test weight was significant for ADG, ABF, LMA and LENGTH. CG by sex interactions were significant for ABF and LMA. No cause was apparent for these interactions. Table 5 lists the regression coefficients of ADG, ABF, LMA and LENGTH on off-test weight. The regression coefficients in Table 5 are very similar to industry estimates from tested market hogs (Goodwin et al., 1989).

Least squares means of barrows and gilts and an estimate of their difference from statistical model 1 are shown in Table 6. Records of ADG, ABF, LMA and LENGTH were adjusted for sex differences before RAM breeding value estimation using additive factors from Goodwin et al. (1987) shown in the Appendix. The additive sex adjustment factors of Goodwin et al. (1987) were derived from littermate pairs of purebred pigs tested during 1980-1985 at the Minnesota central test station. Comparison of the sex adjustment factors used with sex difference estimates from statistical model 1 shows the adjustment factors to be greater than the estimates for ABF, ADG, and LENGTH. The sex adjustment for LMA is similar to the estimate of sex difference.

The effects of sire groups and dam groups were significant for ADG. Table 7 shows the estimates of these differences. Progeny of group 1 sires grew faster than progeny of group 2 sires. Breeders may have given priority to obtaining test station evaluations from their predicted best young sires first. Progeny of group 1 dams grew more slowly than group 2 dams. Possible causes of progeny of older dams growing more rapidly include maternal effects and possible selection bias since previous progeny of older dams have completed records of performance on farm. Sire group by dam group interaction was significant for ADG and LMA. The one estimable function for the interaction was the total of sire group 1 * dam group 1

plus sire group 2 * dam group 2 minus sire group 1 * dam group 2 minus sire group 2 * dam group 1.

Table 4. Analysis of variance of statistical model 1

		P>F			
Source	df	ADG	ABF	LMA	LENGTH
CG	32	.0001	.0001	.0001	.0001
Sex	1	.0001	.0001	.0001	.0001
CG by sex	32	.0529	.0436	.0132	.8000
Sire group	1	.0045	.1632	.7779	.1639
Dam group	1	.0008	.2294	.4599	.5872
Sire group by dam group	1	.0001	.4329	.0481	.3755
Off-test weight	1	.0001	.0001	.0001	.0001
Residual	1321				
R^2		.42	.41	.37	.46
Mean		.825 kg/day	30.1 mm	32.7cm^2	77.1 cm

Table 5. Regressions on off-test weight from statistical model 1

Trait	b	S.E.
ADG, kg/day	.013*	±.00065
ABF, mm	.005*	±.00052
LMA, cm^2	.014*	±.00244
LENGTH, cm	.032*	±.00239

*P<.05.

Table 6. Sex differences from statistical model 1

	Barrow[a]	S.E.	Gilt[a]	S.E.	Difference[b]	S.E.
ADG, kg/day	.845*	±.005	.793*	±.005	.053*	±.006
ABF, mm	30.1*	±.223	28.5*	±.221	1.6*	±.277
LMA, cm^2	31.6*	±.264	35.0*	±.262	-3.4*	±.328
LENGTH, cm	77.0*	±.102	77.7*	±.101	-0.7*	±.126

[a]Least-squares mean.

[b]Estimate of difference between barrows and gilts.

*P<.05.

Table 7. Differences between sire groups and dam groups from statistical model 1

	$\hat{S}1-\hat{S}2$[a]	S.E.	$\hat{D}1-\hat{D}2$[b]	S.E.
ADG, kg/day	.019*	±.007	-.022*	±.006
ABF, mm	.412	±.296	.349	±.290
LMA, cm^2	-.099	±.351	.255	±.344
LENGTH, cm	-.188	±.135	.072	±.133

[a]Sire group 1 - sire group 2.

[b]Dam group 1 - dam group 2.

*P<.05.

The totals are shown in Table 9. The precise interpretation of these totals is not possible without additional information regarding breeder practices of selecting entries for the test station. The sire group by dam group interaction subclass means are shown in Table 8. The assumption of random sampling for the 112 sires and 504 dams in Group 2 listed in Table 3 may be incorrect if their centrally tested progeny were selected as a result of previous progeny on-farm performance.

Table 8. Sire group by dam group interaction least squares means from statistical model 1

Interaction	ADG kg/day	S.E.	ABF mm	S.E.	LMA cm^2	S.E.	LENGTH cm	S.E.
S1 by D1[a]	.830	±.005	29.82	±.21	33.02	±.25	77.27	±.09
S1 by D2[b]	.827	±.004	29.24	±.29	33.44	±.24	77.31	±.09
S2 by D1[c]	.786	±.011	29.18	±.49	33.80	±.59	77.57	±.23
S2 by D2[d]	.833	±.005	29.06	±.22	32.86	±.26	77.38	±.10

[a]Sire group 1 by dam group 1.
[b]Sire group 1 by dam group 2.
[c]Sire group 2 by dam group 1.
[d]Sire group 2 by dam group 2.

Table 9. Totals of sire group by dam group interaction means from statistical model 1

	Total[a]	S.E.
ADG, kg/day	.051*	±.013
ABF, mm	.454	±.578
LMA, cm^2	-1.357*	±.686
LENGTH, cm	-.234	±.264

[a]Total is sire group 1 by dam group 1 minus sire group 1 by dam group 2 minus sire group 2 by dam group 1 plus sire group 2 by dam group 2 interaction means.

*P<.05.

When selection of entries to the test station is based upon prior information about the genetic merit of the parents the expectation of the breeding value of the tested animals is not

zero ($E(\mathbf{u}) \neq 0$) but should be greater than zero. Minnesota test station entry requirements have never included restrictions on the age of the parents. The result is a distribution of parental genetic groups in each contemporary group at the station. Within birth years of parents there may be differences in selection intensity between sires or dams whose tested progeny were selected from their first parity and sires or dams whose first tested progeny were born in later parities when the parents' genetic merit may be known from breeder on-farm records. The magnitude of this difference depends on the knowledge and motives of the breeder.

Table 10 lists the age of parents represented in each CG. Each CG includes tested animals representing different parental genetic groups. Young parents that have no progeny records best fulfill the assumptions of random sampling of parents of tested animals. Table 2 shows 416 of 1498 progeny (28%) would fulfill this random sampling of parents assumption. The Both column of Table 10 shows the distribution by CG of tested animals whose parents fulfill this assumption.

Herd of Origin Differences

Herd of origin (HERD) differences are the result of different management practices, health programs, and selection goals between breeders. In a fixed statistical model genetic differences between herds are also included. HERD differences may provide pre-test environments that influence animal performance at the central test station.

The records of 1498 tested animals with both parents' ages known were evaluated with statistical model 2. The analysis of variance for statistical model 2 is in Table 11. Contemporary group, sex, and sire within herd effects were highly significant for all traits. Beef cattle and swine breeding value estimation procedures routinely account for

Table 10. Parental generation interval represented in each contemporary group

	Sire GI			Dam GI			Total	Known parents		
CG	1[a]	2[b]	3[c]	1	2	3	Pigs[d]	Sire[e]	Dam[f]	Both[g]
1963S	58	16	20	39	4	36	94	94	79	29
1963F	16	10	16	10	15	13	42	42	38	10
1964S	65	20	24	35	18	40	109	109	93	30
1964F	19	20	4	11	5	22	43	43	38	11
1965S	73	24	8	38	13	32	109	105	83	34
1965F	32	19	0	11	22	8	51	51	41	9
1966S	56	15	11	41	13	23	90	82	77	31
1966F	24	16	11	23	10	8	55	51	41	18
1967S	71	27	27	40	26	45	125	125	97	37
1967F	15	27	18	1	21	25	60	60	47	0
1968S	85	15	31	54	6	42	131	131	102	46
1968F	20	29	8	9	23	14	57	57	46	3
1969S	34	16	27	30	8	25	84	77	63	21
1969F	19	28	10	7	17	22	61	57	46	3
1970S	31	16	24	21	7	42	74	71	70	13
1970F	20	19	8	7	16	26	51	47	49	6
1971S	43	14	18	25	17	32	79	75	74	21
1971F	23	24	0	6	12	17	55	47	35	0
1972S	28	16	31	8	14	44	82	75	66	4
1972F	12	4	8	2	10	8	28	24	20	2
1973S	44	11	8	21	6	29	67	63	56	21
1973F	8	8	4	6	0	10	20	20	16	6
1974S	28	4	12	20	6	16	48	44	42	20
1974F	4	8	4	0	11	9	27	16	20	0
1975S	23	4	20	10	4	31	51	47	45	7
1975F	8	11	0	4	0	8	19	19	12	0
1976S	20	4	12	17	8	7	36	36	32	15
1976F	16	0	4	6	4	4	20	20	14	6
1977S	3	7	13	3	0	20	31	23	23	3
1977F	4	7	4	4	4	7	15	15	15	4
1978S	22	8	4	3	8	15	34	34	26	2
1979S	10	16	5	2	6	14	38	31	22	2
1979F	3	0	0	2	1	0	23	3	3	2
1980S	0	0	0	2	2	0	24	0	4	0
1980F	0	0	4	0	3	2	11	4	5	0

[a]Number of tested pigs with parent GI < 1.3 years.
[b]Number of tested pigs with parent GI < 1.8 years but > 1.3 years.
[c]Number of tested pigs with parent GI > 1.8 years.
[d]Total number of pigs tested.
[e]Number of pigs whose sire GI is known.
[f]Number of pigs whose dam GI is known.
[g]Number of pigs tested which have both sire and dam GI < 1.3 years.

these known sources of variation. Contemporary group by sex interaction was statistically significant for ABF (P<.01). The explanation for this interaction is unknown. HERD effects are significant for ABF, LMA, and LENGTH, and approach significance for ADG. Since the traits of ABF, LMA and LENGTH are more highly heritable than ADG the HERD effect may be due in part to genetic differences between herds. The hypothesis of pre-test management and health differences between herds for ADG is not supported by the results of the HERD effect.

Table 11. Analysis of variance of statistical model 2

		P>F				Test
Source	df	ADG	ABF	LMA	LENGTH	Statistics
CG	31	.0049	.0003	.0109	.0031	Residual
Sex	1	.0001	.0001	.0001	.0001	Residual
CG * sex	31	.3551	.0061	.1275	.4581	Residual
HERD	65	.0971	.0001	.0158	.0017	SIRE(HERD)
SIRE(HERD)	262	.0001	.0001	.0001	.0001	Residual
GI	1	.3495	.7674	.4505	.5194	Residual
Residual	1113					
R^2		.54	.71	.57	.56	
MEAN		.82 kg/day	33.8 mm	34.2 cm^2	78.8 cm	

The regression of ADG, ABF, LMA, and LENGTH on mean parental generation interval was included in statistical model 2 in an attempt to account for parity or selection bias effects. The effect of mean parental generation interval was not statistically significant for any trait.

Breeding Value Estimates

Reduced Animal Model differences

Three levels of pedigree information were used in a RAM to estimate breeding values. Four generation pedigrees of the tested animals provided the information. Model 1 included all known ancestors. Model 2 included parents of tested animals and grandparents of tested animals that had no tested progeny. Hence, this model would include maternal grandsires that may provide genetic ties through dams. Model 3 included parents of tested animals only. Model 3 is the most commonly used model for swine breeding data analysis (Mabry, personal communication). Test station records include small samples of each breeder's production. Use of greater amounts of pedigree information may provide more connectedness to the data. The numbers of animals included in each model are shown in Table 12.

Relatively few progeny are tested per parent in central stations. In this study mean number of progeny was 4.8 per sire and 1.6 per dam. The reduction in number of equations by using Model 1 RAM instead of an equivalent animal model is 35%, for Model 2 RAM 40%, and for Model 3 65%. The importance of genetic ties among animals is increased when direct sire or dam connectedness is not extensive. Table 13 lists the direct parent ties by CG. A direct parent tie between CG occurs when a sire or dam is represented by progeny in more than one CG. The largest number of direct ties are among consecutive CG. In CG from 1973 to 1980 relatively fewer direct ties occur due to smaller numbers of animals entered in the station.

Heterogeneous variance

Table 14 shows the product moment correlations between year-season contemporary group phenotypic means and variances. Significant correlations were found for ADG and ABF. Transformation of ADG by natural logarithm and ABF by square

Table 12. Number of animals in additive genetic relationship matrix for three reduced animal models

Animal Birth Year	Tested Animals	Number of animals in relationship matrix: All Model 1	Parents & Grandparents Model 2	Parents Model 3
1955	0	1	0	0
1956	0	9	1	0
1957	0	34	8	0
1958	0	57	17	0
1959	0	120	43	2
1960	0	188	101	16
1961	0	217	138	44
1962	0	295	218	109
1963	140	401	336	236
1964	148	464	385	286
1965	164	501	433	312
1966	141	428	371	262
1967	185	453	419	331
1968	192	438	405	311
1969	141	304	287	232
1970	127	329	321	241
1971	143	267	261	207
1972	107	207	207	178
1973	79	187	184	145
1974	84	175	171	124
1975	61	151	137	107
1976	56	117	109	85
1977	50	90	90	82
1978	44	91	91	86
1979	50	67	67	67
1980	32	37	37	37
Total	1944	5628	4828	3500
Equations[a]		3684	2885	1556

[a]Number of animal equations to be solved in each model.

Table 13. Number of direct parent ties among contemporary groups

YRS[a]	CG	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1963S	1	2	6																
1963F	2		5	2															
1964S	3			4	3	1	1		1										
1964F	4				5	1		1	1										
1965S	5					4	2	1	2	1	1								
1965F	6						5	3	2	3							1		
1966S	7							5	7	6									
1966F	8								4	5	2								
1967S	9									8	6	3		1					
1967F	10										4	1	1	1	1	1			
1968S	11											10	4	1	2	1	1		
1968F	12												6	2	2	2	1	1	
1969S	13													3	5	1			
1969F	14														6	2	2		
1970S	15															6	6		
1970F	16																3	1	
1971S	17																	2	
1971F	18																		2
1972S	19																		
1972F	20																		
1973S	21																		
1973F	22																		
1974S	23																		
1974F	24																		
1975S	25																		
1975F	26																		
1976S	27																		
1976F	28																		
1977S	29																		
1977F	30																		
1978S	31																		
1979S	32																		
1979F	33																		
1980S	34																		
1980F	35																		

[a]Year-season of test, S=spring, F=fall.

20	21	22	23	24	25	26	27	28	29	30	33	32	33	34	35	CG	YRS
																1	1963S
																2	1963F
																3	1964S
																4	1964F
																5	1965S
																6	1965F
																7	1966S
																8	1966F
																9	1967S
																10	1967F
																11	1968S
																12	1968F
																13	1969S
																14	1969F
	1															15	1970S
		1														16	1970F
2	2	1						1								17	1971S
2		1														18	1971F
1	2															19	1972S
		1						1								20	1972F
			1	1												21	1973S
				1												22	1973F
				1	4		1									23	1974S
										1						24	1974F
								1								25	1975S
								1		2						26	1975F
									1	2						27	1976S
										1		1	1			28	1976F
											1					29	1977S
																30	1977F
													2	1		31	1978S
																32	1979S
																33	1979F
																34	1980S
																35	1980F

Table 14. Product moment correlations of contemporary group means and variances

	Variances					
Means	ADG	ABF	LMA	LENGTH	LOG ADG	SQRT ABF
ADG	.348*					
ABF		.362*				
LMA			.289			
LENGTH				.249		
LOG ADG					.134	
SQRT ABF						-.041

*P<.05.

root resulted in mean-variance correlations not different than zero. Breeding values were predicted with RAM Model 3TR from transformed ADG and ABF.

Assumption of constant proportionality between additive genetic and phenotypic variance was necessary when breeding values were predicted since no variance components were estimated from these data.

Comparison of solutions

Product moment correlations (Snedecor and Cochran, 1980) among the three RAM CG solutions are shown in Table 15. The correlations are close to unity and significant among the RAM models.

Table 16 shows the product moment correlations among the phenotypic measurement of a trait and the breeding values estimated by RAM Models 1, 2, and 3. Correlations are close to unity and significant between breeding values from the different RAM models. The correlations between phenotypic measurement and RAM breeding value are consistent for each RAM model within each trait.

Table 15. Product moment correlations of contemporary group solutions from three reduced animal models

ADG	Model 1	Model 2
Model 2	.9999*	
Model 3	.9979*	.9981*
ABF	**Model 1**	**Model 2**
Model 2	.9999*	
Model 3	.9997*	.9997*
LMA	**Model 1**	**Model 2**
Model 2	.9999*	
Model 3	.9995*	.9996*
LENGTH	**Model 1**	**Model 2**
Model 2	.9999*	
Model 3	.9994*	.9994*

*P<.05.

Table 17 shows the rank correlations among predicted breeding values from the three RAM. The rank correlations are close to unity and significant among the three RAM models for all traits.

Mean breeding value rank change

Breeding value rank change is calculated as the absolute value of the difference in rank between two models. Mean breeding value rank change between models is an indication of the importance of model differences. Mean rank change comparisons among models are shown in Table 18 for 3500 animals. For example, in the comparison between Models 1 and 2 for ADG, the average animal ranked 14 places higher or lower. The 3500 animals compared are the parents and progeny included in RAM model 3. Little rank change occurred between RAM models 1 and 2. Apparently the increase in pedigree information is small from Model 2 to Model 1. The increased

Table 16. Product moment correlations of predicted breeding value derived from three reduced animal models

ADG	Actual[a]	Model 1	Model 2	Model 3
Model 1	.8892*			
Model 2	.8884*	.9989*		
Model 3	.8886*	.9889*	.9894*	
Model 3TR[b]	-.8376*	-.9373*	-.9376*	-.9463*
ABF	Actual	Model 1	Model 2	Model 3
Model 1	.6064*			
Model 2	.6073*	.9993*		
Model 3	.6419*	.9847*	.9848*	
Model 3TR[c]	.6453*	.9816*	.9817*	.9974*
LMA	Actual	Model 1	Model 2	
Model 1	.8209*			
Model 2	.8215*	.9994*		
Model 3	.8353*	.9902*	.9904*	
LENGTH	Actual	Model 1	Model 2	
Model 1	.8333*			
Model 2	.8325*	.9991*		
Model 3	.8307*	.9902*	.9905*	

[a]Actual is the phenotypic measurement of the trait.

[b]Model 3 with logarithm transformed ADG. Negative correlations result from correlating log predictors with untransformed predictors.

[c]Model 3 with square root transformed ABF.

*P<.05.

pedigree information in Models 1 and 2 changed the ranking of the animals relative to Model 3. Transformed ABF ranks from Model 3TR showed little change from untransformed ABF ranks but transformed ADG ranks showed larger rank changes when compared to untransformed ADG ranks. The increased pedigree information available in Models 1 and 2 should increase the accuracy of their predictors. Therefore, Models 1 and 2 should be used when extended pedigree information is available.

Table 17. Rank correlations of predicted breeding values from three reduced animal models

ADG	Model 1	Model 2
Model 2	.9968*	
Model 3	.9800*	.9847*
ABF	**Model 1**	**Model 2**
Model 2	.9966*	
Model 3	.9721*	.9780*
LMA	**Model 1**	**Model 2**
Model 2	.9971*	
Model 3	.9802*	.9853*
LENGTH	**Model 1**	**Model 2**
Model 2	.9970*	
Model 3	.9825*	.9873*

*P<.05.

Table 19 shows the mean breeding value rank change for the 402 sires represented in the data. The additional pedigree information in Models 1 and 2 relative to Model 3 changed

Table 18. Mean breeding value rank change among reduced animal models for 3500 animals

Difference	ADG	ABF	LMA	LENGTH
Model 1 - Model 2	14[a]	11	12	13
Model 1 - Model 3	105	126	100	90
Model 2 - Model 3	102	124	98	88
Model 3 - Model 3TR	149	35		

[a]Mean absolute value of difference in rank between models i and j.

Table 19. Mean breeding value rank change among reduced animal models for 402 sires

Difference	ADG	ABF	LMA	LENGTH
Model 1 - Model 2	3[a]	2	2	2
Model 1 - Model 3	18	22	17	15
Model 2 - Model 3	18	22	17	15
Model 3 - Model 3TR	18	4		

[a]Mean absolute value of difference in rank between models i and j.

rankings of sires (5%) more than the 3500 animals in Table 18 (3%). Transforming ADG also changes rankings of sires.

Swine breed associations are publishing test station sire summaries based on solutions from animal models equivalent to Model 3 (Miller, 1988). Other test station data sets should be examined with animal models including extended A^{-1} to determine if rank changes occur.

Environmental and Genetic Trend

Phenotypic trends

The requirements for population change are genetic variation, accuracy of selection, and intensity of selection. The hog population in 1960 had much variation in carcass traits (Hillier, 1961). National breed testing programs were also in place (Boucher, 1960). Christian (1970) stated "the pig has been altered from an animal producing 32% of his carcass weight in closely trimmed ham and loin 10 to 12 years ago to one that today is capable of packing over 40% in these same cuts." He listed the causes of this improvement as nutrition, management, and breeding. Increased feet and leg problems, esophageal ulcers, and stress adaptability problems were also noted.

Phenotypic trend was estimated as the linear regression of an animal's phenotypic measurement on birth year (Snedecor and Cochran, 1980). The regression was weighted by the number of animals within birth year. Table 20 displays the annual trends in performance. The trend for ABF is significant and relatively large. Cumulative change from 1963 to 1980 was -14.8 mm, a reduction in ABF of 36% from the 1963 mean of 41.1 mm. LMA also showed a large significant phenotypic trend. The cumulative increase in LMA was 7.8 square centimeters, an increase of 27% from the 1963 mean of 29.1

Table 20. Phenotypic trends of performance

	b[a]	S.E.
ADG, kg/day	.0008	±.0005
ABF, mm	-.8243*	±.0228
LMA, cm^2	.4307*	±.0239
LENGTH, cm	.1723	±.0093

[a]Regression coefficient of trait on year of test.

*P<.05.

Table 21. Phenotypic means of the Hampshire year-season contemporary groups tested at the Minnesota central test station

YRS[c]	N[d]	ADG[a] kg/day	ABF[b] mm	LMA[b] cm^2	LENGTH[b] cm
1963S	94	.838	40.75	29.41	77.9
1963F	42	.890	40.79	29.67	78.2
1964S	109	.850	41.79	28.83	77.8
1964F	43	.938	40.10	31.48	78.0
1965S	109	.854	40.88	27.75	77.3
1965F	51	.928	38.47	31.15	77.7
1966S	90	.839	38.31	29.99	78.2
1966F	55	.893	40.13	30.57	77.6
1967S	125	.858	37.75	31.02	77.7
1967F	60	.907	37.17	33.02	76.6
1968S	131	.850	35.21	32.83	77.1
1968F	57	.856	35.70	32.77	77.0
1969S	84	.845	35.66	34.44	76.9
1969F	61	.924	34.06	33.48	77.2
1970S	74	.837	33.41	33.80	78.1
1970F	51	.902	33.59	35.27	78.3
1971S	79	.842	33.42	31.19	79.0
1971F	55	.901	32.17	33.76	78.9
1972S	82	.864	31.62	33.22	78.9
1972F	28	.867	28.51	35.72	78.8
1973S	67	.851	29.55	32.08	78.9
1973F	20	.888	32.55	36.24	77.9
1974S	48	.836	30.43	34.12	79.0
1974F	27	.910	33.02	30.90	79.6
1975S	51	.859	31.84	34.77	79.8
1975F	19	.855	31.71	37.41	79.8
1976S	36	.864	30.4	35.71	79.0
1976F	20	.911	32.54	35.86	79.2
1977S	31	.864	30.13	38.16	80.8
1977F	15	.937	31.13	37.28	79.0
1978S	34	.849	28.96	34.56	80.2
1979S	38	.921	31.22	34.38	80.3
1979F	23	.910	28.13	36.96	79.3
1980S	24	.886	29.16	34.04	80.4
1980F	11	.886	30.02	35.40	81.0

[a]ADG was adjusted to a barrow equivalent.

[b]ABF, LMA, and LENGTH were adjusted to a 105 kg barrow equivalent.

[c]Year-season of test where S=spring, F=fall.

[d]Number of Hampshire pigs tested in a year-season.

cm^2. No trend was found for ADG or LENGTH. Phenotypic trend may have environmental and/or genetic components. The year-season (CG) phenotypic means for ADG, ABF, LMA and LENGTH are shown in Table 21.

Smith (1963) found annual phenotypic trend in ABF of -.70 mm in tested Danish Landrace. Cox and Smith (1968) found annual phenotypic trend in ABF of -1.0 mm in Iowa test station animals. Zarnecki (1979) found annual phenotypic trends of .12 cm for LENGTH, .004 kg/day for ADG, -.36 mm for ABF, and .34 cm^2 for LMA in Swedish Landrace. Quijandria et al. (1970), evaluating North Carolina central test station data, reported annual phenotypic trend of -.07 mm for ABF. No significant trend was found for ADG or LMA.

Table 22. Environmental trend estimates from three reduced animal models

ADG	Annual trend[a], kg/day	b[b]	S.E.
Model 1	.0004	.0002	±.0005
Model 2	.0004	.0002	±.0005
Model 3	.0006	.0003	±.0005
ABF	**Annual trend, mm**	**b**	**S.E.**
Model 1	-.8107	-.4053*	±.0276
Model 2	-.8102	-.4051*	±.0276
Model 3	-.7816	-.3908*	±.0279
LMA	**Annual trend, cm^2**	**b**	**S.E.**
Model 1	.4386	.2193*	±.0271
Model 2	.4378	.2189*	±.0271
Model 3	.4242	.2121*	±.0269
LENGTH	**Annual trend, cm**	**b**	**S.E.**
Model 1	.1837	.0918*	±.0099
Model 2	.1837	.0919*	±.0100
Model 3	.1823	.0912*	±.0103

[a]Twice the regression of CG solution on CG.

[b]Regression of CG solution on CG where CG is 6 months.

*P<.05.

Neville et al. (1976) found annual phenotypic trend of -.13 mm for ABF in Georgia test station data. Standal (1979) reported phenotypic trends of -.51 mm for ABF, -.10 cm^2 for LMA, and .019 kg/day in ADG for Norwegian Landrace.

The phenotypic trends of this study are consistent with swine industry goals of reduced ABF and increased LMA (Boucher, 1960).

Environmental trends

Environmental trend represents changes in management practices, nutrition, disease control, and measurement techniques. Estimates of annual environmental trend were calculated as twice the regression of CG solution from RAM on CG. These solutions were doubled since each CG represents a six-month period. Environmental trend estimates from RAM models 1, 2, and 3 are shown in Table 22. ADG showed no significant trend for any RAM. Estimates of environmental trend for ABF, LMA, and LENGTH were highly significant for all RAM. These estimates are of the same sign and similar magnitude as the phenotypic trends in Table 20. Blanchard (1986) reported environmental trend in ADG for centrally tested Hampshire boars.

Genetic trends

Genetic trend was estimated as the linear regression of an animal's estimated breeding value on birth year. The regressions were weighted by number of animals within birth year. The genetic trend estimates are in Table 23. No significant trends were found for ADG, LENGTH, or RAM model 3 LMA. Significant negative genetic trends were found for LMA estimates from RAM 1 and 2. ABF genetic trend estimates were significant, small and positive. Genetic trends of ABF and LMA are small in magnitude and have the opposite sign of phenotypic trends.

Smith (1984) calculated a 1.6% annual genetic change to be possible for percent lean cuts of the carcass. Genetic trend estimates of Model 1 and 2 for ABF are 0.2% of the mean and for LMA 0.1% of the mean but are negative for ABF and LMA.

Table 23. Annual genetic trend estimates from reduced animal models

ADG	b[a], kg/day	S.E.
Model 1	.00012	±.00021
Model 2	.00010	±.00021
Model 3	.00003	±.00021
Model 3TR[b]	-.00007	±.00022
ABF	**b, mm**	**S.E.**
Model 1	.06389*	±.01194
Model 2	.06344*	±.01194
Model 3	.03822*	±.01190
Model 3TR[c]	.00299*	±.00100
LMA	**b, cm²**	**S.E.**
Model 1	-.02552*	±.01185
Model 2	-.02463*	±.01186
Model 3	-.01311	±.01185
LENGTH	**b, cm**	**S.E.**
Model 1	-.00487	±.00477
Model 2	-.00459	±.00477
Model 3	-.00387	±.00474

[a]Regression of breeding value on the birth year of animal.

[b]Model 3 with log transformed ADG.

[c]Model 3 with square root transformed ABF.

*P<.05.

Cox and Smith (1968) reported a .49 mm annual genetic increase in ABF of Iowa Hampshires. Zarnecki (1979) reported annual genetic trends of .009 kg/day for ADG, .32 cm for LENGTH, -.70 mm for ABF and .59 cm^2 for LMA in Swedish centrally tested pigs. Standal (1979) found annual genetic trend of -.35 mm in Norwegian Landrace. Lundeheim and Eriksson (1984) reported annual genetic trends of centrally tested Swedish Landrace and Yorkshires to be .005 kg/day for ADG, -.47 mm for ABF, and -.16 cm for LENGTH. Kennedy et al. (1986) reported an annual genetic trend of .03 mm for ABF in Canadian Hampshires. Blanchard (1986) did not find any genetic trends in centrally tested Hampshire boars.

The sum of the environmental trends and genetic trends equal the phenotypic trends. Small differences are due to rounding trend estimates. The large environmental trends found in Table 22 suggest much of the phenotypic trends in ABF and LMA found in Table 20 are due to factors other than genetics of the animals. Traits with high heritability, such as ABF and LMA, would be expected to have a large genetic component in the phenotypic trend if breeders are selecting for ABF and LMA throughout the period. Genetic groups were not included in the RAM due to data confounding. If older animals were overevaluated the genetic trend estimates would be reduced (Bichard et al., 1973). It is likely that older animals have been overevaluated since there are phenotypic trends for ABF and LMA.

The genetic trends of ABF and LMA in this study closely resemble the results of Cox and Smith (1968). They also found large phenotypic trends and small genetic trends of the opposite sign. Smith (1963) also reported genetic trend for ABF one-fifth as large as the phenotypic trend. He suspected the assumptions needed of his data to justify the trend estimation methods used had been violated. He listed the possible causes of data differences to be:

1) breeder goals and policies of test station participation may differ;
2) differences in breeders' expertise in selection of entries;
3) overlapping generations over the period in which trend is occurring;
4) maternal effects on test station performance.

Cox and Smith (1968) discuss the "dilemma" of not knowing whether their phenotypic or genetic trend estimates correctly describe the population change. This study is faced with the same dilemma.

CONCLUSIONS

Minnesota Hampshire central testing station data were chosen for evaluation because extensive pedigree information was available, the station was not changed physically during the period considered, diets were relatively constant throughout the test period, many breeders entered pigs during most or all of the period considered, and highly heritable traits were measured.

Inbreeding coefficients for 98% of the tested animals were zero or less than .05. Hence, mixed model procedures that utilize Henderson's simple method of $\mathbf{A}^{-1}$ calculation would be appropriate for these data.

Parents of tested animals may have come from different genetic subpopulations if genetic trend was occurring in the Hampshire hog population. Positive assortative mating by age was evident among parents of tested animals. Sires and dams of similar age were most often mated.

Tested pigs from dams whose first tested progeny were from the dam's second or later parity grew faster than those of first parity dams. There may be a need for age of dam adjustments or the dams may have been selected on prior on-farm progeny performance.

Tested pigs from sires whose first tested progeny were entered in the test station during the sire's first season of production grew faster than tested pigs of sires represented initially in the station in their second or later season of use. Test station results were widely published. Breeders may have preferred to test progeny of their better young boars as soon as possible to secure advertising for on-farm breeding stock sales.

Herd of origin effects were found for ABF, LMA, and LENGTH. It was not possible to determine the exact causes of these differences among herds. Possible causes include differences in weaning practices, disease status, and genetic differences.

Comparison of three levels of pedigree information suggests the merit of using an extended $\mathbf{A}^{-1}$ for test station data evaluation. A typical animal model evaluation includes pedigree information for tested animals and their parents. Whereas, an extended $\mathbf{A}^{-1}$ could include pedigree information for grandparents without tested progeny, parents of tested animals, and the tested animals. A benefit of an extended $\mathbf{A}^{-1}$ for swine central test data evaluation is to provide genetic ties among the dams through maternal grandsires.

Mean breeding value rank changes between RAM were largest when grandparent information was added to the $\mathbf{A}^{-1}$. Mean breeding value rank changes were proportionately larger for the 402 sires than for all 3500 animals evaluated. If sire rankings are a goal of genetic evaluation the rank changes resulting from additional pedigree information may be important. Further investigation of extended relationship matrices for test station data is warranted. Genetic trend estimates changed slightly when $\mathbf{A}^{-1}$ was extended with grandparent pedigree information.

Transformation of ADG resulted in greater mean rank changes than the addition of grandparent pedigree information. Other swine central test station data should be evaluated with transformed data models to assess the importance of heterogeneous variance within contemporary groups. Transformation of ABF caused small changes in mean breeding value rank.

Phenotypic trends of ABF and LMA are large and significant. No trend was found for ADG or LENGTH. The trends for ABF and LMA reflect the selection goals of the swine industry in 1963.

Environmental trends for ABF, LMA, and LENGTH are large and significant, nearly equalling the phenotypic trends.

Estimates of genetic trend for all traits are small. Only ABF and LMA are significant. Possible reasons for small estimates include no real genetic trend in the population,

incorrect heritability may have been used in the RAM to predict breeding values, use of 1980s adjustment factors for pigs born in the 1960s may have been inappropriate, changing goals within the swine industry during the period considered, and biased genetic evaluations. Sources of genetic evaluation bias include:

1) genetic groups were not included in the RAM when $\mathbf{A}^{-1}$ did not extend to the base Hampshire population;
2) genetic variance and/or heritability may have changed during the eighteen year period;
3) pigs entered may not be representative of a sire's progeny;
4) if selection of parents has occurred based on farm records there is no way to know what the selection process was or incorporate the selection matrix (L') into the evaluation.

The possibility that these RAM Minnesota swine test station data evaluations are not BLUP reduces confidence in the estimates of genetic trend. Confounding within these data limited the RAM that could be solved. There may have been genetic trend occurring that would have been found with a RAM that included genetic groups. The use of an $\mathbf{A}^{-1}$ that has been altered to make progeny proven parents fixed as in Henderson (1988) may be closer to the true model.

When test station programs are structured to meet mixed model data assumptions the animal model is an excellent tool. The correct testing procedures to produce unbiased data have been known for at least 35 years. Current U.S. test station programs do not require random sampling of entries or restrict age of parents. The data that result from these programs have a greater possibility of having confounding of genetic groups with contemporary groups if there are few tested animals within a contemporary group. Test stations should also require as complete pedigree information as possible. Lack of pedigree information may become a cause of genetic group confounding for small contemporary groups. Phantom genetic

groups to account for missing pedigree information are less useful when contemporary group size is small. Central test stations should encourage large single breed contemporary groups with known pedigrees to reduce the chances of data confounding.

Cooperation between central test supervisors, swine breeders, and genetic evaluators will lead to more accurate genetic evaluations using an animal model.

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APPENDIX

Adjustments to 105 kg (Weber, 1987)

ABF=

$$\left[\text{actual ABF} + \left[(230 - \text{final wt.}) * \frac{\text{actual ABF}}{(\text{final wt.} - 25)}\right]\right] * 25.4$$

LMA=

$$\left[\text{actual LMA} + \left[(230 - \text{final wt.}) * \frac{\text{actual LMA}}{(\text{final wt.} + 155)}\right]\right] * 6.45$$

$$\text{LENGTH} = \left[\text{actual LENGTH} + \left[(230 - \text{final wt.}) * 0.033\right]\right] * 2.54$$

Adjustment factors added to gilt records to obtain barrow equivalent (Goodwin et al., 1987).

ABF	+2.80 mm	LMA	-3.225 square cm
ADG	+0.077 kg/day	LENGTH	-1.32 cm